I. CLAIM AMENDMENT

Please amend the claims as indicated below:

1. (Currently amended) A method for introducing into a ~~naturally non-isoflavonoid-producing~~ plant species the enzyme catalyzing the aryl migration of a flavanone to form an isoflavanone intermediate or an isoflavone, comprising:

introducing a DNA segment encoding said enzyme into said plant to form a transgenic plant, wherein said transgenic plant expresses said DNA segment under the control of a suitable constitutive or inducible promoter when said transgenic plant is exposed to conditions which permit expression.

2. (Previously presented) The method of Claim 1, wherein chalcone synthase, chalcone reductase, and chalcone isomerase genes are also expressed in said plant to cause in vivo formation of daidzein or a daidzein derivative.

3. (Previously presented) The method of Claim 2, wherein said plant is further transformed to comprise said chalcone synthase, chalcone reductase, and chalcone isomerase genes.

4. (Previously presented) The method of Claim 1 or 2, wherein said plant further comprises downstream genes to metabolize said formed isoflavanone intermediate or isoflavone to biologically active isoflavonoid derivatives or conjugates.

5. (Previously presented) The method of Claim 4, wherein said downstream gene is selected from the group consisting of isoflavone *O*-methyltransferase, isoflavone 2'-hydroxylase, isoflavone reductase, and vestitone reductase.

6. (Previously presented) The method of Claim 5, wherein said plant comprises down-stream gene 4'-*O* methyltransferase to form biochanin A or a biochanin A derivative.

7. (Currently amended) <u>The method of claim 1,</u>~~A method for increasing the level of isoflavonoid compounds in~~ <u>wherein the plant is a</u> naturally isoflavonoid-producing plants ~~comprising:~~

~~introducing a DNA segment encoding the enzyme catalyzing the aryl migration of a flavanone to yield an isoflavonoid to form a transgenic plant~~, wherein said transgenic plant expresses said DNA segment under the control of a suitable constitutive or inducible promoter when said transgenic plant is exposed to conditions which permit expression and wherein the plant exhibits increased levels of isoflavonoid compounds from the expression.

8. (Previously presented) The method of Claim 7, wherein said isoflavonoid is selected from the group consisting of an isoflavonone intermediate, an isoflavone, an isoflavone derivative, and an isoflavone conjugate.

9. (Currently amended) The method of Claim 1 ~~or 7~~, wherein said DNA segment comprises isolated genomic DNA.

10. (Currently amended) The method of Claim 1 ~~or 7~~, wherein said DNA segment comprises recombinant cDNA.

11. (Currently amended) The method of Claim 1 ~~or 7~~, wherein said DNA segment comprises CYP93C gene.

12. (Currently amended) The method of Claim 11, wherein said gene consists of the sequence from nucleotide 36 to nucleotide 1598 of the sequence depicted in SEQ ID NO: 1.

13. (Currently amended) The method of Claim 1 ~~or~~ 7, said DNA segment is a *Medicago truncatula* homolog of a CYP93C gene.

14. (Previously presented) The method of Claim 12, wherein said gene consists of the sequence from nucleotide 92 to nucleotide 1657 of the sequence depicted in SEQ ID NO:4.

15. (Currently amended) The method of Claim 8 ~~1 or 7~~, wherein said flavanone is liquiritigenin.

16. (Currently amended) The method of Claim 8 ~~1 or 7~~, wherein said flavanone is naringenin.

17. (Currently amended) The method of Claim 1 ~~or 7~~, wherein said transgenic plant possesses an isoflavonoid which is isolated from said plant and used to prepare a food.

18. (Currently amended) The method of Claim 1~~or 7~~, wherein said transgenic plant possesses an isoflavonoid which is isolated from said plant and used to prepare a food stuff, a nutritional supplement, an animal feed supplement, a nutraceutical, or a pharmaceutical.

19. (Currently amended) The method of Claim 1~~or 7~~, wherein said transgenic plant possesses an isoflavonoid which provides a pharmaceutical benefit to a patient.

20. (Previously presented) A method for synthesizing an isoflavanone intermediate or an isoflavone from a flavanone by expressing a recombinant CYP93C gene segment in a suitable bacterial, fungal, algal, or insect cell system.

21. (Previously presented) A method of reducing the levels of isoflavonoid compounds in a naturally isoflavonoid-producing plant comprising introducing and expressing an antisense or gene silencing construct that contains an intact CYP93C gene or segments thereof into said plant.

22. (Previously presented) The method of Claim 20 or 21, wherein said gene consists of the sequence from nucleotide 36 to nucleotide 1598 of the sequence depicted in SEQ ID NO:1.

23. (Previously presented) The method of Claim 20 or 21, wherein said gene consists of the sequence from nucleotide 92 to nucleotide 1657 of the sequence depicted in SEQ ID NO:4.

24. (Previously presented) A naturally non-isoflavonoid producing plant cell transformed by introducing a DNA a segment encoding the enzyme catalyzing the aryl migration of a flavanone to form an isoflavanone intermediate or an isoflavone, wherein said transgenic plant cell expresses said DNA segment under the control of a suitable constitutive or inducible promoter when exposed to conditions which 5 permit expression.

25. (Previously presented) The plant cell of Claim 24, wherein chalcone synthase, chalcone reductase, and chalcone isomerase genes are also expressed in said plant to cause in vivo formation of daidzein or a daidzein derivative.

26. (Previously presented) The plant cell of Claim 25, wherein said plant cell is further transformed to comprise said chalcone synthase, chalcone reductase, and chalcone isomerase genes.

27. (Previously presented) The plant cell of Claim 24 or 25, wherein said plant cell further comprises downstream genes to metabolize said formed intermediate or isoflavone to biologically active isoflavonoid derivatives or conjugates.

28. (Previously presented) The plant cell of Claim 27, wherein said downstream gene is selected from the group consisting of isoflavone *O*-methyltransferase, isoflavone 2'-hydroxylase, isoflavone reductase, and vestitone reductase.

29. (Previously presented) The plant cell of Claim 28, methyltransferase to form biochanin A in said plant cell comprises downstream gene 4'-0-A derivative.

30. (Previously presented) A naturally isoflavonoid-producing plant cell transformed by introducing a DNA segment encoding the enzyme catalyzing the aryl migration of a flavanone to yield an isoflavonoid to form a transformed plant cell, wherein said transformed plant cell expresses said DNA segment under the control of a suitable constitutive or inducible promoter when exposed to conditions which permit expression.

31. (Previously presented) The plant cell of Claim 30, in said isoflavonoid is selected from the group isoflavone, an isoflavone derivative, and an consisting of an isoflavonone isoflavone conjugate.

32. (Previously presented) The plant cell of Claim 24, 30 or 31, wherein said DNA segment comprises isolated genomic DNA.

33. (Previously presented) The plant cell of Claim 24, 30 or 31, wherein said DNA segment comprises recombinant cDNA.

34. (Previously presented) The plant cell of Claim 24, 30 or 31, wherein said DNA segment comprises CYP93C gene.

35. (Previously presented) The plant cell of Claim 34, wherein said DNA segment consists of the sequence from nucleotide 36 to nucleotide 1598 of the sequence depicted in SEQ ID NO: 1.

36. (Previously presented) The plant cell of Claim 24, 30 or 31, wherein said DNA segment is a *Medicago truncatula* homolog of a CYP93C gene.

37. (Previously presented) The plant cell of Claim 36, wherein said gene consists of the sequence from nucleotide 92 to nucleotide 1657 of the sequence depicted in SEQ ID N0:4.

38. (Previously presented) A transgenic plant cell having reduced levels of isoflavonoid compounds, said plant cell transformed by introducing an antisense or gene silencing construct that contains an intact CYP93C gene or segments thereof into said plant cell.

39. (Previously presented) The plant cell of Claim 38, wherein said gene consists of the sequence from nucleotide 36 to nucleotide 1598 of the sequence depicted in SEQ ID NO: 1.

40. (Previously presented) The plant cell of Claim 38, wherein said gene consists of the sequence from nucleotide 92 to nucleotide 1657 of the sequence depicted in SEQ ID NO:4.

41. (Previously presented) An isolated gene or DNA segment comprising a portion which encodes a cytochrome P450 of the CYP93 family that can catalyze the aryl migration of a flavanone to yield an isoflavanone intermediate or an isoflavone, wherein said portion consists of nucleotide 36 to nucleotide 1598 of the sequence depicted in SEQ ID NO: 1.

42. (Previously presented) The gene or DNA segment of Claim 41, wherein said gene is the soybean gene encoding the enzyme catalyzing the aryl migration of liquiritigenin.

43. (Previously presented) The gene or DNA segment of Claim 41, wherein said gene is the soybean gene encoding the enzyme catalyzing the aryl migration of naringenin.

44. (Previously presented) A protein encoded by a portion of an isolated gene or DNA segment which encodes a cytochrome P450 that can catalyze the aryl migration of a flavanone to yield an isoflavanone intermediate or an isoflavone, wherein said portion consists of nucleotide 36 to nucleotide 1598 of the sequence depicted in SEQ ID NO: 1.

45. (Previously presented) An isolated gene or DNA segment comprising a portion which encodes a cytochrome P450 that can catalyze the aryl migration of a flavanone to yield an isoflavanone intermediate or an isoflavone, wherein said portion is a *Medicago truncatula* homolog of a CYP93C gene.

46. (Previously presented) The gene or DNA segment of Claim 45 consisting of nucleotide 92 to nucleotide 1657 of the sequence depicted in SEQ ID NO:4.

47. (Previously presented) The gene or DNA segment of Claims 45 or 46, wherein said gene is the *Medicago truncatula* gene encoding the enzyme catalyzing the aryl migration of liquiritigenin.

48. (Previously presented) The gene or DNA segment of Claims 45 or 46, wherein said gene is the *Medicago truncatula* gene encoding the enzyme catalyzing the aryl migration of naringenin.

49. (Previously presented) A protein encoded by a portion of an isolated gene or DNA segment which encodes a cytochrome P450 that can catalyze the aryl migration of a flavanone to yield an isoflavanone intermediate or an isoflavone, wherein said portion is a *Medicago truncatula* homolog of a CYP93C gene.

50. (Previously presented) A transgenic plant transformed with an isolated gene or DNA segment which encodes a cytochrome P450 that can catalyze the aryl migration of a flavanone to yield an isoflavanone intermediate or an isoflavone, wherein said transgenic plant exhibits increased levels of an isoflavonoid when compared to the level of said isoflavonoid in plants of the same species which do not comprise said isolated gene or DNA segment.

51. (Previously presented) The transgenic plant of Claim 50, wherein the level of bacterial or fungal symbiosis is increased.

52. (Previously presented) The transgenic plant of Claim 50, wherein at least a portion of said transgenic plant is made into a composition suitable for ingestion as a food stuff, a nutritional supplement, an animal feed supplement, or a nutraceutical.

53. (Previously presented) The transgenic plant of Claim 50, wherein at least a portion of said edible transgenic plant material capable of being ingested for its nutritional value is made into a food.

54. (Previously presented) A method of preparing a nutraceutical composition for achieving a nutritional effect using a transgenic plant transformed with an isolated gene or DNA segment

which encodes a cytochrome P450 that can catalyze the aryl migration of a flavanone to yield an isoflavanone intermediate or an isoflavone, wherein said transgenic plant exhibits increased levels of an isoflavonoid when compared to the level of said isoflavonoid in plants of the same species which do not comprise said isolated gene or DNA segment.

55. (Previously presented) A method of preparing a pharmaceutical composition for achieving a therapeutic effect using a transgenic plant transformed with an isolated gene or DNA segment which encodes a cytochrome P450 that can catalyze the aryl migration of a flavanone to yield an isoflavanone intermediate or an isoflavone, wherein said transgenic plant exhibits increased levels of an isoflavonoid when compared to the level of said isoflavonoid in plants of the same species which do not comprise said isolated gene or DNA segment.

56. (Previously presented) A method of using a transgenic plant transformed with an isolated gene or DNA segment which encodes a cytochrome P450 that can catalyze the aryl migration of a flavanone to yield an isoflavanone intermediate or an isoflavone, wherein said transgenic plant exhibits increased levels of an isoflavonoid when compared to the level of said isoflavonoid in plants of the same species which do not comprise said isolated gene or DNA segment to provide a nutraceutical benefit to a human or animal administered said isoflavonoid.

57. (Previously presented) The method of Claim 56, wherein said isoflavonoid is administered by ingestion of at least a portion of said plant.

58. (Previously presented) The method of Claim 56, wherein said isoflavonoid is administered by ingestion of a composition comprising an isoflavonoid isolated from said plant.

59. (Previously presented) A method of transforming a plant with an isolated gene or DNA segment which encodes a cytochrome P450 that can catalyze the aryl migration of a flavanone to yield an isoflavanone intermediate or an isoflavone, wherein said transgenic plant exhibits increased levels of an isoflavonoid when compared to the level of said isoflavonoid in plants of the same species which do not comprise said isolated gene or DNA segment.

60. (Previously presented) The method of Claim 59, wherein the nutritional value of said plant is increased.

61. (Previously presented) The method of Claim 59, wherein the disease resistance in said plant is increased.

62. (Previously presented) The method of Claim 59, wherein bacterial or fungal symbiosis in said plant is increased.

63. (Previously presented) The method of claim 59, wherein said plant is a leguminous plant.

64. (Previously presented) The method of claim 63, wherein the nodulation efficiency of said plant is increased.

65. (Previously presented) A leguminous transgenic plant exhibiting increased nodulation efficiency, wherein said transgenic plant is transformed with an isolated gene or DNA segment which encodes a cytochrome P450 that can catalyze the aryl migration of a flavanone to yield an isoflavanone intermediate or an isoflavone, wherein said transgenic plant exhibits increased levels of an isoflavonoid when compared to the level of said isoflavonoid in plants of the same species which do not comprise said isolated gene or DNA segment.

66. (Previously presented) A transgenic plant comprising at least one recombinant DNA sequence encoding a cytochrome P450 that can catalyze the aryl migration of a flavanone to yield an isoflavanone intermediate or an isoflavone, wherein said transgenic plant exhibits an increased level of an isoflavonoid when compared to the level of said isoflavonoid in plants of the same species which do not comprise said recombinant DNA sequence.

67. (Previously presented) Seed from a transgenic plant comprising at least one recombinant DNA sequence encoding a cytochrome P450 that can catalyze the aryl migration of a flavanone to yield an isoflavanone intermediate or an isoflavone, wherein said transgenic plant exhibits an increased level of an isoflavonoid when compared to the level of said isoflavonoid in plants of the same species which do not comprise said recombinant DNA sequence.

68. (Previously presented) Progeny from a transgenic plant comprising at least one recombinant DNA sequence encoding a cytochrome P450 that can catalyze the aryl migration of a flavanone to yield an isoflavanone intermediate or an isoflavone, wherein said transgenic plant

exhibits an increased level of an isoflavonoid when compared to the level of said isoflavonoid in plants of the same species which do not comprise said recombinant DNA sequence.

69. (Previously presented) Progeny from seed of a transgenic plant comprising at least one recombinant DNA sequence encoding a cytochrome P450 that can catalyze the aryl migration of a flavanone to yield an isoflavanone intermediate or an isoflavone, wherein said transgenic plant exhibits an increased level of an isoflavonoid when compared to the level of said isoflavonoid in plants of the same species which do not comprise said recombinant DNA sequence.

RESPONSE TO RESTRICTION REQUIREMENT

As an initial matter, Applicants note that the Restriction appears to have been established with respect to the earlier amended claims from the PCT application, claim 1-65, and not the claims submitted in the Preliminary Amendment filed concurrently with the case, claims 1-69. Applicants respectfully request that the current claims be considered. Applicants nonetheless provide the comments below with respect to the pending claims in order to speed the prosecution of the case. It is respectfully requested that these comments be taken into consideration prior to issuance of a new restriction based on the amended claims. The comments have also been provided to ensure the responsiveness of this communication.

In response to the Restriction which the Examiner imposed, Applicants elect, with traverse, the Group I claims, claims 1-6, 9-11, 13-14, 17, 19-24, 27-29, 32 and 34-36.

Under the lack of unity standard, unity of invention has to be considered in the first place only in relation to the independent claims in an international application and ***not the dependent claims***. See M.P.E.P. §1850. Under this standard there is not a lack of unity even if a dependent claim itself contains a further invention. Currently, each of claims 1-19 as amended herein depend from claim 1 and therefore, on this basis alone, must be considered together. Applicants therefore respectfully request that originally identified Groups I, II, and IV-VII be considered together.

As to the original division of Groups I from II; IV from V; and VI from VII, these were made based on the recitation of either SEQ ID NO:1 or SEQ ID NO:4 in a dependent claim. As indicated above, this is improper because it is based on limitations found only in a dependent claim. It is additionally improper because the Commissioner has decided *sua sponte* to partially waive 37 CFR 1.475 and 1.499 et seq. to permit applicants to claim up to ten (10) nucleotide

sequences even when not having the same or corresponding special technical feature without the payment of an additional fee, although such a common technical feature is present here. See M.P.E.P. §1850. As stated in M.P.E.P. §1850, for example:

> The PCT permits inventions that lack unity of invention to be maintained in the same international application for payment of additional fees. Thus, in international applications, for each group for which applicant has paid additional international search and/or preliminary examination fees, the USPTO has determined that up to ***four (4)*** such additional sequences per group is a ***reasonable number*** for examination. Further, claims directed to the selected sequences ***will be examined*** with claims drawn to any sequence combinations which have a common technical feature with the selected sequences. Nucleotide sequences encoding the same protein are considered to satisfy the unity of invention standard and will continue to be examined together.
>
> *Id.* (emphasis added)

Here, only two sequences are involved. The division of the claims on this basis is therefore improper and, Groups I and II; IV and V; and VI and VII must be considered together even before considering the remainder of the claims.

With regard to the relation between Group I-II and IV-V, it is noted that both claims already included the same method step found in their main independent claims, claims 1 and 7, respectively. This limitation is as follows:

> introducing a DNA segment encoding said enzyme into said plant to form a transgenic plant, wherein said transgenic plant expresses said DNA segment under the control of a suitable constitutive or inducible promoter when said transgenic plant is exposed to conditions which permit expression.

While the preamble of claim 1 refers to "A method for introducing into a naturally non-isoflavonoid-producing plant species the enzyme catalyzing the aryl migration of a flavanone to form an isoflavanone intermediate or an isoflavone" and the preamble of claim 7 refers to "A method for increasing the level of isoflavonoid compounds in naturally isoflavonoid-producing plants," the fact that the claims included the same method step makes them indivisible under lack of unity practice as they share this same ***common technical feature***. In order to further clarify

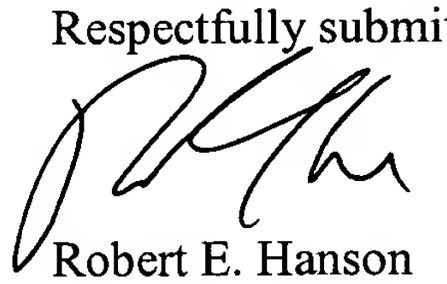
this and simplify the claim structure, Applicants have amended claim 1 so that it is generic to claims 1 and 7. The shared common technical feature is even more clear and thus the claims share unity.

Finally, as for the assertion that the inventive concept is found in the prior art, it is noted that the IPER specifically acknowledged the novelty and inventive step of the claims. *See* IPER Section V. As noted in the IPER, the prior art does not teach any function for CYP93C1. The common technical feature of the claims therefore is *prima facie* inventive and links all of the claims.

In view of the foregoing, Applicants respectfully submit that the claims identified in Groups I, II, and IV-VII must be considered together. In view of the inventive common technical feature, it is respectfully submitted that the remaining claims should be examined together in a second grouping.

The Examiner is invited to contact the undersigned attorney at (512) 536-3085 with any questions, comments or suggestions relating to the referenced patent application.

Respectfully submitted,



Robert E. Hanson
Reg. No. 42,628
Attorney for Applicants

FULBRIGHT & JAWORSKI L.L.P.
600 Congress Avenue, Suite 2400
Austin, Texas 78701
(512) 536-3085

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